

--Figure 1A, comprising Figures 1A-1 to 1A-8, is a series of representative LOH analysis results obtained using tissue samples obtained from two patients, designated E26 and E46. Figures 1A-1, 1A-3, 1A-5, and 1A-7 depict results from tissue obtained from patient E26. Figures 1A-2, 1A-4, 1A-6, and 1A-8 depict results from tissue obtained from patient E46. In each figure, fluorescent PCR products were generated by amplification of DNA obtained from normal (N) and tumor (T) tissue samples from the corresponding patient, and products were separated by size. For each tracing, the horizontal axis represents DNA fragment size, and the vertical axis (i.e. peak height) represents relative amount of each fragment. Several fragment sizes (in base pairs) are indicated.--

Please delete the paragraph beginning at page 16, line 11 and ending at page 16, line 25, and substitute the following paragraph therefor.

-- Figure 3B, comprising Figures 3B-1 to 3B-4, is a series of sequence chromatograms of *FEZ1* genes obtained from three individuals having mutated *FEZ1* genes, represented by SEQ ID NOs: 65 to 71. As indicated in Figure 3B-2 (SEQ ID NO: 66), a point mutation in *FEZ1* (TCC/Ser → CCC/Pro) at codon 29 was identified in ~~an~~ a primary esophageal cancer tissue sample obtained from patient E44. Nucleotide sequences from normal DNA from patient E44 (N) and from a BAC contig (B) are shown for comparison. A bold line overlies the altered codon. In a primary esophageal cancer tissue sample obtained from patient E50, a point mutation in *FEZ1* (AAG/Lys → GAG/Glu) was detected at codon 119 was found, as indicated in Figure 3Biv. The normal BAC sequence chromatogram is shown in Figure 3B-3 (SEQ ID NO: 67). A third point mutation in *FEZ1* (CAG/Gln → TAG/STOP) at codon 501 was identified in prostate cancer cell line PC3, as indicated in Figure 3B-6 (SEQ ID NO: 70), in which the sequence chromatogram 3'- to 5'- direction. Repeated sequencing indicated the presence of a weak signal corresponding to guanine (G) within a large adenine (A) signal in the first nucleotide at codon 501, suggesting that a fraction of the cancer cells retained the normal *FEZ1* allele. Figure 3B-1, 3B-4, and 3B-5 represent SEQ ID NOs: 65, 68, and 69, respectively. --

In the Claims:

Kindly amend claims 100-102, 112, 113, 123, 135, 136, and 140 as follows.